AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

235. A method for identifying a compound that putatively elicits or modulates human T1R1 receptor polypeptide-associated taste in a human subject based on its effect on T1R1 polypeptide activation comprising:

(1) screening one or more compounds in a functional assay that detects compounds which activate a human T1R1 receptor polypeptide or detect compounds that modulate (enhance or inhibit) the activation of a human T1R1 polypeptide by another compound wherein said T1R1 polypeptide is selected from the group consisting of:

(a) a T1R1 polypeptide having the amino acid sequence contained in any one of SEQ. ID. NO: 17;

(b) a human T1R1 polypeptide that possesses at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 17;

(c) a human T1R1 polypeptide which is encoded by a nucleic acid sequence that hybridizes to the T1R1 polypeptide coding region of the nucleic acid sequence contained in SEQ. ID. NO: 16 or SEQ. ID. No: 17 under stringent hybridization conditions or a functional fragment thereof which is encoded by a portion of said coding region which is at least 500 nucleotides in length;

(d) a human T1R1 polypeptide that is a functional fragment of a T1R1 polypeptide according to (a) or (b);

(2) identifying compounds from step (1) that putatively elicit or modulate T1R1 polypeptide-associated taste based their (a) activation or modulation (inhibition or enhancement) of the activation of a T1R1 polypeptide according to (a), (b), (c), or (d), by another compound in said functional assay.

236. The method of claim 235, wherein said T1R1 polypeptide has the amino acid sequence contained in SEQ. ID. NO: 17.

237. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 90% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

238. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 95% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

239. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 96% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

240. The method of claim 235, wherein the T1R1 polypeptide possesses at least 97% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

241. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 97% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

242. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 98% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

243. The method of claim 235, wherein said T1R1 polypeptide has an amino acid sequence that possesses at least 99% sequence identity to the polypeptide contained in SEQ. ID. NO: 17.

244. The method of claim 235, wherein said T1R1 polypeptide is encoded by a nucleic acid sequence that hybridizes to the T1R1 coding region contained in SEQ. ID. NO: 15 or 16 under stringent hybridization conditions.

245. The method of claim 235, wherein said T1R1 polypeptide comprises a functional fragment of the polypeptide contained in SEQ. ID. No: 17.

246. The method of claim 235, wherein said T1R1 polypeptide is expressed by a cell.

247. The method of claim 235, wherein said cell is intact or permeabilized.

248. The method of claim 235, wherein said T1R1 polypeptide is comprised in a membrane extract.

249. The method of claim 246, wherein said T1R1 polypeptide is expressed on the surface of said cell.

250. The method of claim 246, wherein the cell is a prokaryotic cell.

251. The method of claim 246, wherein the cell is a eukaryotic cell.

252. The method of claim 251, wherein said cell is a yeast, insect, amphibian or mammalian cell.

253. The method of claim 252, wherein the cell is a CHO, HEK-293, COS or Xenopus oocyte.

254. The method of claims 246, wherein said cell further expresses a G protein.

255. The method of claim 254, wherein said G protein is $G_{\alpha 15}$ or $G_{\alpha 16}$ or gustducin.

256. The method of claim 235, wherein said functional assay detects the effect of said compound on phosphorylation of the T1R1 polypeptide.

257. The method of claim 235, wherein the functional assay detects the effect of said compound on the dissociation of said T1R1 polypeptide and a G protein.

258. The method of claim 235, wherein the functional assay detects the effect of said compound on arrestin translocation.

259. The method of claim 235, wherein the functional assay detects the effect of said compound on second messengers.

260. The method of claim 235, wherein the functional assay detects the effect of said compound on signal transduction.

261. The method of claim 235, wherein the functional assay is a transcriptional assay.

262. The method of claim 235, wherein said functional assay comprises a GTPγ^{35}S assay.

263. The method of claim 259, wherein said functional assay detects changes in cAMP, cGMP or IP3.

264. The method of claims 235, wherein said functional assay determines whether said component results in a detectable change in intracellular calcium.

265. The method of claim 264, which uses a calcium-sensitive dye.

266. The method of claim 235 which detects the effect of said compound on G protein activation of said T1R1 polypeptide.

267. The method of claim 265, wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

268. The method of claim 235, wherein said T1R1 polypeptide in said functional assay is stably or transiently expressed by a cell.

269. The method of claim 235, wherein the functional assay detects changes in ionic polarization of a cell or membrane that expresses the T1R1 polypeptide.

270. The method of claim 268, wherein ion polarization is detected by a voltage-clamp or patch-clamp method.

271. The method of claim 235, wherein said functional assay comprises a radiolabeled ion flux assay or fluorescence assay that detects T1R1 activity using a voltage-sensitive dye.

272. The method of claim 235, wherein said assay comprises a fluorescent polarization or FRET assay.

273. The method of claim 235, wherein said assay detects changes in adenylate cyclase activity.

274. The method of claim 235, wherein the functional assay detects a change in ligand dependent coupling of said T1R1 polypeptide with a G protein.

275. The method of claim 274, wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

276. The method of claim 235, wherein said functional assay detects changes in intracellular cAMP or cGMP.

277. The method of claim 235, wherein said assay measures the effect of said compound on transmitter or hormone release.

278. The method of claim 235 wherein said functional assay detects the effect of said compound on the transcription of a gene of interest.

279. The method of claim 278, wherein said gene is a reporter selected from chloramphenicol acetyltransferase, luciferase, 3'-galactosidase and alkaline phosphatase.

280. The method of claim 235, wherein the functional assay is a high throughput assay.

281. The method of 280, wherein said functional assay screens a library of compounds.

282. The method of claim 281, wherein said library is a combinatorial chemical library.

283. The method of claim 282, wherein said library comprises at least 1000 compounds.

284. The method of claim 235, wherein the effect of said putative T1R1 taste modulator is assayed in vivo for its effect on T1R1 receptor polypeptide-associated taste.

285. The method of claim 284 which assays the effect of said compound on the taste of a particular compound.

286. The method of claim 285, wherein said assay detects the effect of said compound on a sweet or umami tasting compound.

IN THE TITLE:

Delete the title and substitute the following:

TITLE:

- Functional Assays That Use The T1R1 Receptor to Screen for TIR1-Associated Taste Modulators -